

APPROVED	O.G. FIG.
BY	CLASS SUBCLASS
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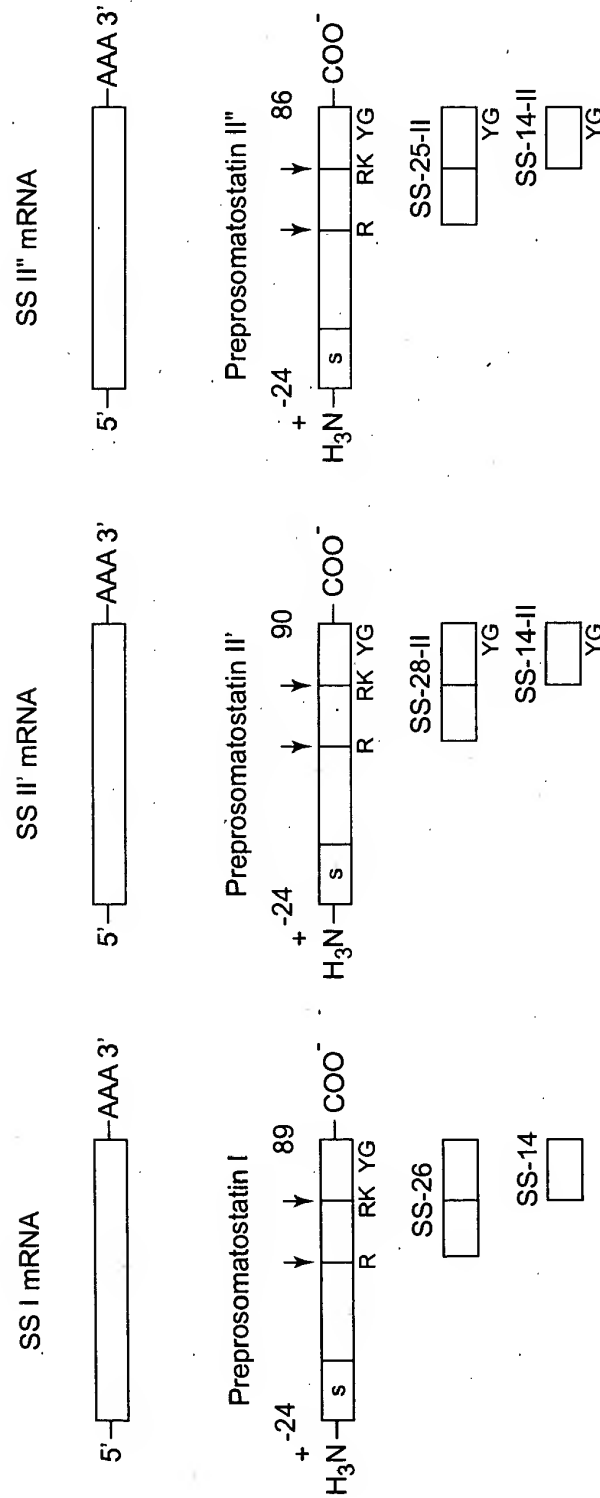


Fig. 1

APPROVED	O.G. FIG.
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[illegible]

PPSS-I

SEQ ID NO: 8	5'GGGGGGGGGGAACAGGAGCAGCAGAACTCAAAGAGAGAGCCAATCTCAACGATTGCTGCCCCAATTGAACCACTTTATCC	81
	ATCCTCTGCCTCCCCGAGACCCAGAGAAG ATG CTC TCG ACG CGT GTC CAG TGC GCC CTA GCA CTA CTC	152
	SEQ ID NO: 3	Met Leu Ser Thr Arg Val Gln Cys Ala Leu Ala Leu Leu
	158	
	TCC CTA GCC CTG GCC ATC AGC AGC GTC TCT GCC GCT CCG TCC GAT GCC AAA CTC CGC CAG CTG	214
	Ser Leu Ala Leu Ala Ile Ser Ser Val Ser Ala Ala Pro Ser Asp Ala Lys Leu Arg Gln Leu	67
	CTC CAA CGG TCA CTC ATG GCA CCT GCA GGC AAA CAG GAG CTT GCC AGG AAT ACA CTC GTA GAG	272
	Leu Gln Arg Ser Leu Met Ala Pro Ala Gly Lys Gln Glu Leu Ala Arg Asn Thr Leu Val Glu	46
	CTA CTC TCA GAG CTC GCA CAT GTA GAG AAC GAG GCG ATT GAA TTG GAT GAC ATG TCT CAT GGC	340
	Leu Leu Ser Glu Leu Ala His Val Glu Asn Glu Ala Ile Glu Leu Asp Asp Met Ser His Gly	25
	GTG GAG CAG GAG GAT GTG GAT CTC GAG CTG GAG CGT GCA CCC GGC CCA GTA CTG GCT CCA CGT	403
	Val Glu Gln Glu Asp Val Asp Leu Glu Leu Glu Arg Ala Pro Gly Pro Val Leu Ala Pro Arg	4
	GAA CGC AAG GCT GGA TGC AAG AAC TTC TTC TGG AAG ACC TTT ACA TCG TGT TAA TGAATCTACTC	466
	Glu Arg Lys Ala Gly Cys Lys Asn Phe Phe Trp Lys Thr Phe Thr Ser Cys ***	
	CTTTACTGTGTACTACATCTCATCTCTTTTGTGTTTCAATCACTCATTTGCTGAATCCAAATGCACCATGGCCTAACCCCTCTCT	549
	TCAAAAATTTAAATAAACACGTGTTATTAACTTTAAACAATCATCTGATGTTTCTATCGCTCACTAGATTTTTTCCGAAAAG	632
	GAACACAAGAAAGATGTTCTACAAATGTATGCGGTTCTGCTTTGACTGTGATTATGATTTATTTGGCAGACTATTTTTTAATTG	715
	TTTGTGTTGAATAAAATCTGTGTTTCAGAAACCAAAAAAATAAAAAA 3'	

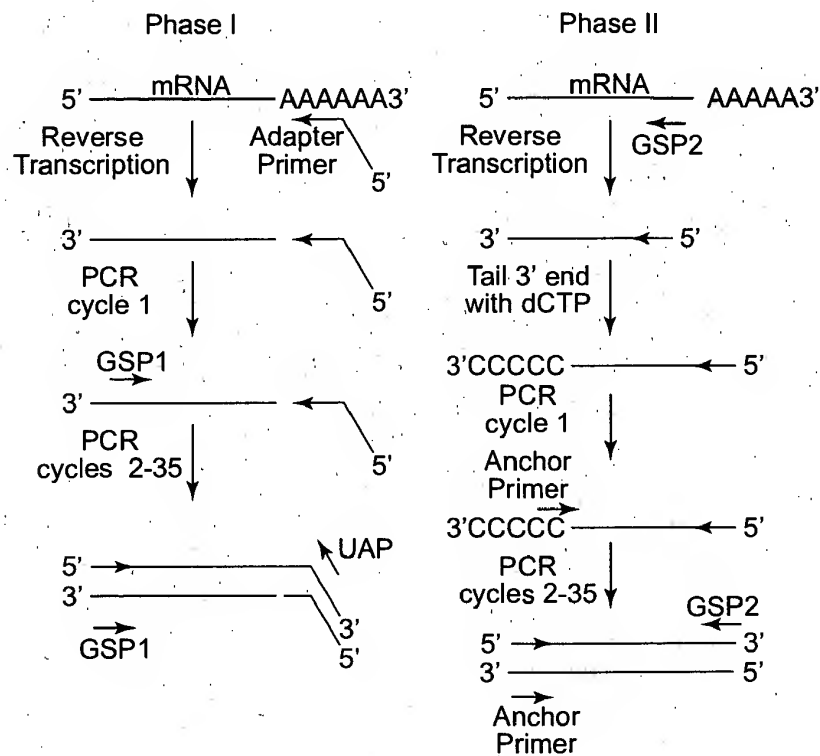
Fig. 2

APPROVED	O.G. FIG.
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PPSS-II' and PPSS-II"	
SEQ ID NO: 14 PPSS-II'	accaggcctgctccataccagctgagcagatccagcgggtccagctcagctgctcaccgcgtgcca 75
SEQ ID NO: 20 PPSS-II"	accaggcctgctccataccagctgagcagatccagcgggtccagctcagctgctcaccgcgtgcca 70
SEQ ID NO: 9 Lys Cys Arg	
PPSS-II'	tccctgcaaaacacccagctctgttgag ATG AAG GTC TGC CGA ATC CAC TGT GCC CTG GCC 139/-91
PPSS-II"	tccctgcaaaacacccagctctgttgag ATG AAG GTC TGC CAA ATC CAC TGT GCA CTG GCC 134/-87
SEQ ID NO: 15 Met Arg Val Ser Gln Ile His Cys Ala Leu Ala	
PPSS-II'	CTG CTG GGT TTG GCC CTG GCC ATT TGC AGC CAA GGA GCC GCC TCG CAG CCC GAC CTG 196/-72
PPSS-II"	CTG CTG GGT TTG GCC CTG GCC ATT TGC AGC CAA GGA GCC GCC TCG CAG CCA GAC CTG 191/-68
Leu Leu Gly Leu Ala Leu Ala Ile Cys Ser Gln Gly Ala Ala Ser Gln Pro Asp Leu	
Arg	
PPSS-II'	GAC CTC GCG AGC CGC AGA CTC CTT CAG AGG GCT CGT GCC GCT GCA TTG CCA CAC AGG 253/-53
PPSS-II"	GAC CTC GCG AGC CGC CGA CTC CTC CAG AGG GCC CTG GCC GCT GCA TTG CCA CAC AGG 248/-49
Asp Leu Ala Ser Arg Arg Leu Leu Gln Arg Ala Leu Ala Ala Leu Pro His Arg	
PPSS-II'	AGT GGA GTA AGC GAG CGG TGG AGG ACA TTC TAT CCC AAC TGT CCT TGC CTG *** 304/-35
PPSS-II"	AGT GGA GTA AGC GAG CGA TGG AGG ACA TTC TAT CCC AAC TGT CCT TGC CTG AGG TGG 305/-30
Ser Gly Val Ser Glu Arg Trp Arg Thr Phe Tyr Pro Asn Cys Pro Cys Leu Arg Trp	
Cys	
PPSS-II'	AGG CCC AGG AAA GTG AAG TGT CAA *** GCG GGG GCT AAA GAG GAC CTG CGT GTG GAG 358/-18
PPSS-II"	AGG CCC AGA AAA GTG AAG GGT CCA CAG CTG AAG GCC AAA GAG GAC *** *** 350/-14
Arg Pro Arg Lys Val Lys Gly Pro Gln Leu Lys Ala Lys Glu Asp	
Gly Asn Pro Asn	
PPSS-II'	CTG GAG CGC TCA GTG GGC AAC CCC AAC AAC CTT CCC CCC CGT GAG CGC AAA GCC GGC 415/+2
PPSS-II"	CTG GAG CGC TCA GTG GAC *** *** AAC CTT CCC CCC CGC GAG CGC AAA GCT GGC 398/+2
Leu Glu Arg Ser Val Asp	
Asn Leu Pro Pro Arg Glu Arg Lys Ala Gly	
PPSS-II'	TGC AAG AAC TTC TAC TGG AAG GGC TTC ACT TCC TGC tga gggagaataaacccgaccacatt 477
PPSS-II"	TGC AAG AAC TTC TAC TGG AAG GGA TTC ACT TCT TGC taa gggagaataaacccgaccacatt 460
Cys Lys Asn Phe Tyr Trp Lys Gly Phe Thr Ser Cys ###	
PPSS-II'	atgacatgacgtgccaatcacgtcacacccgccaacttacacctgacgaatgcagccaatcaacagttagctgtg 552
PPSS-II"	atgacacaatgcattcaatcacatcacacccgccaacttacacctgacgaatgcagccaatcaacagttagctgtg 535
cccgatgatggttcttgaaatacaacagaaatgatgtacctgtctaatgttgaaataaaataataattg(a)n	
PPSS-II'	cctgatgacaattatgattatgatgtacctgactaatttagaataaagagagaataaaggagaac(a)n

Fig. 3

APPROVED	O.G. FIG.
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*Fig. 4*

APPROVED	O.G. FIG.
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Nucleotide Identity

TRI	82.8	49.0	43.7	52.3	51.0	52.0	51.5	51.1	52.8	54.5
84.1	TRI	48.2	39.1	44.9	50.0	50.0	49.5	48.0	49.8	52.5
45.5	43.9	TRI	58.1	77.0	67.7	68.9	67.9	69.4	69.4	72.5
35.6	35.6	52.3	AFI	60.1	58.8	55.1	53.8	55.3	56.8	56.8
44.7	40.9	73.5	52.3	CFI	65.7	68.7	67.7	68.4	67.7	72.2
47.7	44.7	70.5	49.2	64.4	TRI	75.0	74.5	62.6	75.5	78.3
42.4	38.6	66.7	46.2	63.6	78.8	CFI	84.1	84.3	84.3	84.3
42.4	38.6	65.2	45.5	62.9	78.0	87.9	TR	92.4	91.2	92.2
42.4	38.6	66.7	46.2	63.6	78.8	88.6	97.0	B	94.4	95.5
42.4	38.6	64.4	46.2	62.9	78.8	90.9	96.2	98.5	M	98.7
45.5	42.4	73.5	47.7	68.2	87.1	91.7	97.7	98.5	100	TH

Amino Acid Identity

Fig. 5

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FIG. 6

Comparison of Amino Acid Sequences of Peptides Derived from Preprosomatostatin Ia

	-20	-10	+1	+10	+14	SEQ ID NO:
Rainbow trout ^b						4
Hagfish ^d						27
Lamprey ^d						1
Torpedo ^d						28
Ratfish ^d						29
Bowfin ^d						30
Sturgeon ^d						1
Catfish ^d						31
Salmon ^d						2
Anglerfish ^c						2
Eel ^d						1
Flounder ^d						1
Sculpin ^d						2
Frog ^c						2
Salamander ^d						1
Alligator ^d						1
Pigeon ^d						1
Ovine ^d						32

Fig. 6

APPROVED	O.G. FIG.
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FIG. 7

Sequence comparison

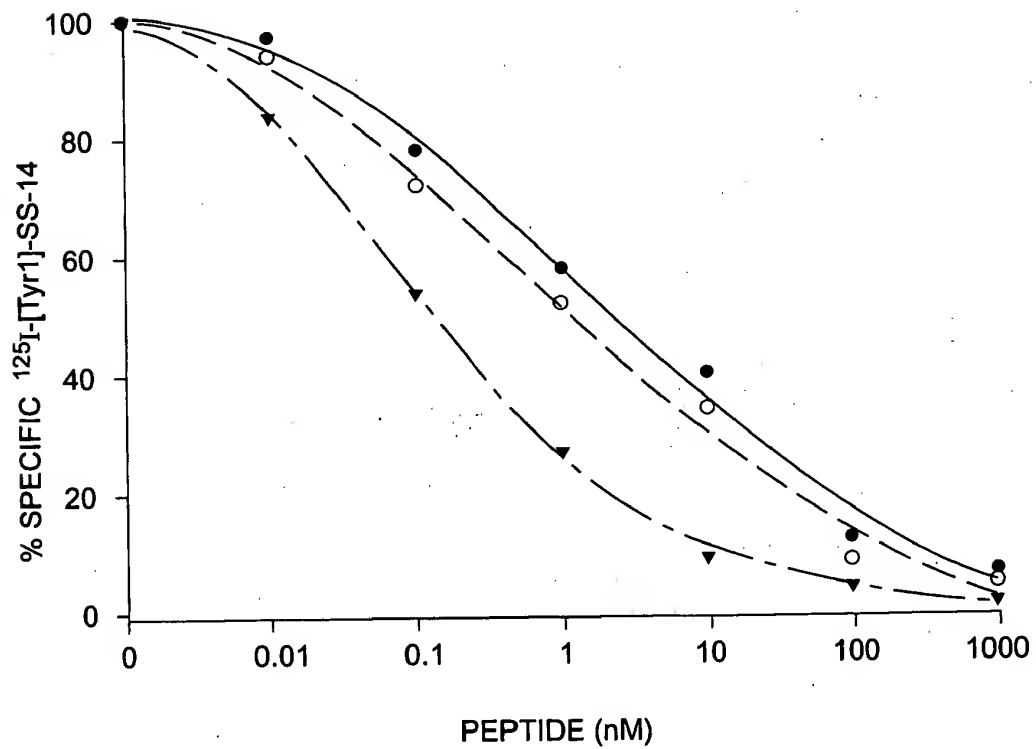
SEQ ID NO: 9	TRII'	---	MKVCRIHCALALLGLALAIACSQASQP	---	DLDRSRRLQARAAAAPHRSVGSER
SEQ ID NO: 15	TRII"	---	MRVSQIHCALALLGLALAIACSQASQP	---	DLDRSRRLQARAAAAPHRSVGSER
SEQ ID NO: 36	CFII	---	MSSSPLRALALMCLVSAVGVISGRP	---	HVLNSALEARNVPFGVEVPERLT
SEQ ID NO: 37	AFII	---	MQCIRCPAILALLVLCPGVSQDLREQSDNQDLLELRQHWLLERARSAGLLSQEWSKRA	---	DLFRHRLQARASATQATQDFTKRD
SEQ ID NO: 38	GFII	---	MRLCELCYLLALLGLSLVLCGRCAQL	---	EP
SEQ ID NO: 39	GFIII	---	---	---	PVEERNPAQSRELSKE-RKELILKL
SEQ ID NO: 40	FRII	---	---	---	PDDNRITTTGRNQDLNAIQDILLKL
SEQ ID NO: 3	TRI	---	---	---	DAKLQQLQSLMAPAGKQELARNT
SEQ ID NO: 41	CFI	---	---	---	DAKLQQLQSLMAPAGKQELARNT
SEQ ID NO: 42	AFI	---	---	---	DAKLQQLQSLMAPAGKQELARNT
SEQ ID NO: 43	GFI	---	---	---	DAKLQQLQSLMAPAGKQELARNT
SEQ ID NO: 44	FRI	---	---	---	DAKLQQLQSLMAPAGKQELARNT
SEQ ID NO: 45	C	---	---	---	DAKLQQLQSLMAPAGKQELARNT
SEQ ID NO: 46	R	---	---	---	DAKLQQLQSLMAPAGKQELARNT
SEQ ID NO: 47	B	---	---	---	DAKLQQLQSLMAPAGKQELARNT
SEQ ID NO: 48	M	---	---	---	DAKLQQLQSLMAPAGKQELARNT
SEQ ID NO: 49	H	---	---	---	DAKLQQLQSLMAPAGKQELARNT

(continued)

WRTFYPNCPCLR--PRKVKCP-AGAKE-DLR--VELERSVGN-PNNLPPRERKAGCKNFYWKGFSTSC
WRTFYPNCPCLRWRPRKVKGPQLKAKE-DL-----ERSV-----DNLPPrERKAGCKNFYWKGFSTSC
LPELQW-MLSNNELTPVQVEEAPRS-----RLELVRDN-----T-VTSKPLNCMNIFYWKSRTAC
VEELAQMSLPEATFOREAEDASWATE-G-----RMNLEERSVDS-TNNLPPrERKAGCKNFYWKGFSTSC
VEKLILLSIPMEMR--EKGLSMAGE-SEDLRLQEERSAES-SNQLPTRVRKEGCKNFYWKGFSTSC
ISGLD--GVDNSVLDGEIAPVPDAEPELESRL-ERAVYNRLSQLPQDRKAPCKNFYWKGFSTSC
LSGWTID-S-RESNLVEVERNVDPPE-P-----KIPPSVK--FPRLSLRERKAPCKNFYWKGFSTSC
LVELLS-ELAHVENEAEIELDDMSHVE-QEDVDLELERAPG--PVLAPRERKAGCKNFYWKGFSTSC
LAELLA-ELAEAEENEVIDSDSDEVSRAAE-SEGARLEMERAG--PVLAPRERKAGCKNFYWKGFSTSC
LAELLSDLQGENEAELEENFPLAEGGPDADHADLERASG-GPLAPRERKAGCKNFYWKGFSTSC
LADLLS-ELVQAEAEAELEPEDLSRAVE-KDEVRLERLEAAG--PMLAPRERKAGCKNFYWKGFSTSC
LAELLS-EPQOTNEAELESDDLPRGAE-QDEVRLERLEAAG--PMLAPRERKAGCKNFYWKGFSTSC
LAELLS-EPQOTNEAELESDLSRGAE-QDEVRLERLEAAG--PMLAPRERKAGCKNFYWKGFSTSC
LAELLS-EPNQTENDALEPEDLPQAAE-QDEMRLERLQRSANS-NPAMAPRERKAGCKNFYWKGFSTSC
LAELLS-EPNQTENDALEPEDLSQAAE-QDEMRLERLQRSANS-NPAMAPRERKAGCKNFYWKGFSTSC
LAELLS-EPNQTENDALEPEDLSQAAE-QDEMRLERLQRSANS-NPAMAPRERKAGCKNFYWKGFSTSC
LAELLS-EPNQTENDALEPEDLSQAAE-QDEMRLERLQRSANS-NPAMAPRERKAGCKNFYWKGFSTSC

Fig. 7

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*Fig. 8*